

SEQUENCE LISTING

<110> Choe, Sunghwa  
Feldmann, Kenneth A

<120> Dwf7 MUTANTS

<130> 2225-0003

<140> 09/775,879

<141> 2001-02-02

<150> 60/179,901

<151> 2000-02-02

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<170> PatentIn Ver. 2.0

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25

<210> 2

<211> 26

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<213> Artificial Sequence

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ggaaagatca tcaaacattt acatgt

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<210> 3

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aagtatagtt gggttccggc gaggtta 26

<210> 11  
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<210> 13  
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<212> DNA  
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<210> 14  
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<210> 15  
 <211> 364  
 <212> PRT  
 <213> delta-7 sterol C-5 desaturase (*Candida glabrata*)

<400> 15  
 Met Asp Leu Val Leu Glu Thr Leu Asp His Tyr Ile Phe Asp Asp Val  
 1                   5                   10                   15

Tyr Ala Lys Ile Ala Pro Val Glu Leu Gln Arg Gly Ile Asp Asp Ser  
 20                   25                   30

Leu Val Asn Ala Leu Ser Leu Asn Lys Ile Val Ser Asn Ser Thr Leu  
 35                   40                   45

Leu His Glu Thr Leu Ser Ile Thr Asn Ser Leu Lys Arg Val Asn Lys  
 50                   55                   60

Asp Val Tyr Gly Leu Thr Pro Phe Leu Phe Asp Phe Thr Glu Lys Thr  
 65                   70                   75                   80

Tyr Ala Ser Leu Leu Pro Arg Asn Asn Leu Ile Arg Glu Phe Phe Ser  
 85                   90                   95

Leu Trp Ala Val Val Thr Val Phe Gly Leu Leu Leu Tyr Leu Ile Thr  
 100                105                110

Ala Ser Leu Ser Tyr Val Phe Val Phe Asp Arg Thr Ile Phe Asn His  
 115                120                125

Pro Lys Tyr Leu Lys Asn Gln Met Tyr Leu Glu Ile Lys Leu Ala Val  
 130                135                140

Ser Ala Ile Pro Thr Met Ser Leu Leu Thr Val Pro Trp Phe Met Leu  
 145                150                155                160

Glu Leu Asn Gly Tyr Ser Lys Leu Tyr Tyr Asp Val Asp Trp Glu His  
 165                170                175

His Gly Leu Arg Lys Leu Leu Ile Glu Tyr Ala Thr Phe Ile Phe Phe  
 180                185                190

Thr Asp Cys Gly Ile Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg

195	200	205
Val Tyr Lys Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr		
210	215	220
Pro Phe Ala Ser His Ala Phe His Pro Val Asp Gly Tyr Phe Gln Ser		
225	230	235
Leu Ser Tyr His Ile Tyr Pro Met Ile Leu Pro Leu His Lys Ile Ser		
245	250	255
Tyr Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Ser Val Met Ile His		
260	265	270
Asp Gly Gln His Met Ser Asn Asn Pro Val Val Asn Gly Thr Ala Cys		
275	280	285
His Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr		
290	295	300
Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Glu Asp Ser		
305	310	315
Leu Phe Asp Pro Lys Leu Lys Met Asp Lys Lys Val Leu Glu Lys Gln		
325	330	335
Ala Arg Glu Thr Ala Ala Tyr Ile Gln Glu Val Glu Gly Asp Asp Thr		
340	345	350
Asp Arg Val Tyr Asn Thr Asp Lys Lys Lys Thr Asn		
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<212> PRT		
<213> delta-7 sterol C-5 desaturase ( <i>Saccharomyces cerevisiae</i> )		
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1	5	10
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20	25	30
Trp Gln Lys Leu Leu Gly Leu Asn Ser Gly Phe Ser Asn Ser Thr Ile		
35	40	45
Leu Gln Glu Thr Leu Asn Ser Lys Asn Ala Val Lys Glu Cys Arg Arg		
50	55	60
Phe Tyr Gly Gln Val Pro Phe Leu Phe Asp Met Ser Thr Thr Ser Phe		
65	70	75
		80

Ala Ser Leu Leu Pro Arg Ser Ser Ile Leu Arg Glu Phe Leu Ser Leu  
                   85                         90                         95  
  
 Trp Val Ile Val Thr Ile Phe Gly Leu Leu Leu Tyr Leu Phe Thr Ala  
                   100                     105                     110  
  
 Ser Leu Ser Tyr Val Phe Val Phe Asp Lys Ser Ile Phe Asn His Pro  
                   115                     120                     125  
  
 Arg Tyr Leu Lys Asn Gln Met Ala Met Glu Ile Lys Leu Ala Val Ser  
                   130                     135                     140  
  
 Ala Ile Pro Trp Met Ser Met Leu Thr Val Pro Trp Phe Val Met Glu  
                   145                     150                     155                 160  
  
 Leu Asn Gly His Ser Lys Leu Tyr Met Lys Ile Asp Tyr Glu Asn His  
                   165                     170                     175  
  
 Gly Val Arg Lys Leu Ile Ile Glu Tyr Phe Thr Phe Ile Phe Phe Thr  
                   180                     185                     190  
  
 Asp Cys Gly Val Tyr Leu Ala His Arg Trp Leu His Trp Pro Arg Val  
                   195                     200                     205  
  
 Tyr Arg Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro  
                   210                     215                     220  
  
 Phe Ala Ser His Ser Phe His Pro Val Asp Gly Phe Leu Gln Ser Ile  
                   225                     230                     235                 240  
  
 Ser Tyr His Ile Tyr Pro Leu Ile Leu Pro Leu His Lys Val Ser Tyr  
                   245                     250                     255  
  
 Leu Ile Leu Phe Thr Phe Val Asn Phe Trp Thr Val Met Ile His Asp  
                   260                     265                     270  
  
 Gly Gln Tyr Leu Ser Asn Asn Pro Ala Val Asn Gly Thr Ala Cys His  
                   275                     280                     285  
  
 Thr Val His His Leu Tyr Phe Asn Tyr Asn Tyr Gly Gln Phe Thr Thr  
                   290                     295                     300  
  
 Leu Trp Asp Arg Leu Gly Gly Ser Tyr Arg Arg Pro Asp Asp Ser Leu  
                   305                     310                     315                 320  
  
 Phe Asp Pro Lys Leu Arg Asp Ala Lys Glu Thr Trp Asp Ala Gln Val  
                   325                     330                     335  
  
 Lys Glu Val Glu His Phe Ile Lys Glu Val Glu Gly Asp Asp Asn Asp  
                   340                     345                     350  
  
 Arg Ile Tyr Glu Asn Asp Pro Asn Thr Lys Lys Asn Asn  
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<210> 17  
<211> 329  
<212> PRT  
<213> delta-7 sterol C-5 desaturase (*Schizosaccharomyces pombe*)

<400> 17  
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Tyr Gly Lys Ile Ala Glu Ser Phe Asp Ser Ser Ser Phe Ala Asn  
20 25 30  
Thr Ala Val Asn Ser Thr Thr Leu Gly Leu Ala Glu Lys Val Asn Phe  
35 40 45  
Ala Ile Thr Ser Gly Leu Leu Asp Arg Asn Asn Val Trp Arg Gln Phe  
50 55 60  
Thr Ser Leu Phe Leu Ile Thr Trp Ile Met Gly Thr Leu Ser Tyr Phe  
65 70 75 80  
Leu Ser Ala Ser Phe Ala Tyr Tyr Val Tyr Phe Asp Arg Glu Glu Ala  
85 90 95  
Arg Arg His Pro Lys Phe Leu Lys Asn Gln Glu His Leu Glu Leu Met  
100 105 110  
Val Ala Leu Lys Asn Leu Pro Gly Met Ala Ile Leu Thr Ala Pro Trp  
115 120 125  
Phe Leu Ala Glu Ile Arg Gly Tyr Gly Tyr Val Tyr Asp Lys Leu Asp  
130 135 140  
Glu Tyr Gly Tyr Phe Tyr Leu Phe Phe Ser Ile Ala Leu Phe Leu Leu  
145 150 155 160  
Phe Ser Asp Phe Leu Ile Tyr Trp Ile His Arg Ala Leu His His Arg  
165 170 175  
Trp Leu Tyr Ala Pro Leu His Lys Leu His His Lys Trp Ile Val Pro  
180 185 190  
Thr Pro Tyr Ser Ser His Ala Phe His Tyr Leu Asp Gly Tyr Ser Gln  
195 200 205  
Ser Leu Pro Tyr His Met Phe Pro Phe Phe Pro Leu Asn Lys Tyr  
210 215 220  
Val Tyr Leu Leu Leu Phe Gly Ser Val Asn Tyr Trp Thr Val Leu Ile  
225 230 235 240  
His Asp Gly Lys Tyr Phe Ser Asn Asn Ala Val Val Asn Gly Ala Ala  
245 250 255

His	His	Ala	Ala	His	His	Met	Tyr	Phe	Asn	Tyr	Asn	Tyr	Gly	Gln	Phe
						260		265					270		
Phe	Thr	Leu	Phe	Asp	Arg	Leu	Cys	Ser	Ser	Tyr	Arg	Gln	Pro	Asp	Gln
	275					280				285					
Glu	Leu	Phe	Asp	Ala	Glu	Leu	Arg	Asn	Glu	Lys	Leu	Gln	Glu	Gln	Arg
	290				295					300					
Ile	Arg	Phe	Met	Glu	Thr	Val	Gln	Tyr	Thr	Val	Glu	Gly	Lys	Asp	Asp
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Arg	Thr	Tyr	Ala	Ser	Lys	Lys	Asp	Asn							
				325											

<210> 18  
<211> 281  
<212> PRT  
<213> DWF7/STE1 (Arabidopsis)

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Phe	Tyr	Asn	Arg	Ile	Val	Leu	Ser	His	Leu	Leu	Pro	Ala	Asn	Leu	Trp
		20					25					30			
Glu	Pro	Leu	Pro	His	Phe	Leu	Gln	Thr	Trp	Leu	Arg	Asn	Tyr	Leu	Ala
		35					40				45				
Gly	Thr	Leu	Leu	Tyr	Phe	Ile	Ser	Gly	Phe	Leu	Trp	Cys	Phe	Tyr	Ile
		50				55				60					
Tyr	Tyr	Leu	Lys	Ile	Asn	Val	Tyr	Leu	Pro	Lys	Asp	Ala	Ile	Pro	Thr
		65				70			75			80			
Ile	Lys	Ala	Met	Arg	Leu	Gln	Met	Phe	Val	Ala	Met	Lys	Ala	Met	Pro
			85					90			95				
Trp	Tyr	Thr	Leu	Leu	Pro	Thr	Val	Ser	Glu	Ser	Met	Ile	Glu	Arg	Gly
			100				105				110				
Trp	Thr	Lys	Cys	Phe	Ala	Ser	Ile	Asp	Glu	Phe	Gly	Trp	Ile	Leu	Tyr
		115					120				125				
Phe	Val	Tyr	Ile	Ala	Ile	Tyr	Leu	Val	Phe	Val	Glu	Phe	Gly	Ile	Tyr
		130				135				140					
Trp	Met	His	Arg	Glu	Leu	His	Asp	Ile	Lys	Pro	Leu	Tyr	Lys	Tyr	Leu
		145			150				155			160			
His	Ala	Thr	His	His	Ile	Tyr	Asn	Lys	Gln	Asn	Thr	Leu	Ser	Pro	Phe
			165					170			175				

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro  
                  180                     185                 190  
  
 His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile  
                  195                     200                 205  
  
 Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys  
                  210                     215                 220  
  
 Ile His Gly Asn Ile Trp Pro Val Met Gly Ala Gly Tyr His Thr Ile  
                  225                     230                 235                 240  
  
 His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met  
                  245                     250                 255  
  
 Asp Trp Met Phe Gly Ser Leu Arg Asp Pro Leu Leu Glu Glu Ásp Asp  
                  260                     265                 270  
  
 Asn Lys Asp Ser Phe Lys Lys Ala Glu  
                  275                     280  
  
  
 <210> 19  
 <211> 291  
 <212> PRT  
 <213> delta-7 sterol C-5 desaturase concensus  
  
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     20                 25                     30  
  
 Leu Glu Thr Leu Asn Lys Val Asn Tyr Gly Pro Phe Leu Phe Asp Phe  
     35                 40                     45  
  
 Thr Glu Thr Ser Phe Ser Leu Leu Pro Arg Asn Asn Leu Trp Arg Glu  
     50                 55                     60  
  
 Phe Leu Ser Leu Trp Leu Ile Val Thr Ile Phe Gly Leu Leu Tyr Ile  
     65                 70                     75                 80  
  
 Ala Ser Leu Ser Tyr Phe Phe Asp Ile Phe Asn His Pro Lys Tyr Leu  
     85                 90                     95  
  
 Lys Asn Gln Met Leu Glu Ile Lys Ala Val Ala Ile Pro Trp Met Ser  
    100                 105                     110  
  
 Leu Leu Thr Val Pro Trp Phe Met Glu Leu Gly Tyr Ser Lys Leu Tyr  
    115                 120                     125  
  
 Lys Ile Asp Glu His Gly Arg Lys Leu Phe Ile Glu Ala Thr Phe Phe  
    130                 135                     140

Phe Thr Asp Gly Ile Tyr Ala His Arg Trp Leu His Trp Pro Tyr Lys  
 145 150 155 160  
 Ala Leu His Lys Pro His His Lys Trp Leu Val Cys Thr Pro Phe Ala  
 165 170 175  
 Ser His Ala Phe His Pro Val Asp Gly Tyr Leu Gln Ser Leu Tyr His  
 180 185 190  
 Ile Tyr Pro Leu Leu Pro Leu His Lys Ser Tyr Leu Leu Phe Thr Phe  
 195 200 205  
 Val Asn Phe Trp Thr Val Met Ile His Asp Gly Gln Ser Asn Asn Pro  
 210 215 220  
 Val Val Asn Gly Ala Cys His Thr Val His His Leu Tyr Phe Asn Tyr  
 225 230 235 240  
 Asn Tyr Gly Gln Phe Thr Thr Leu Trp Asp Arg Leu Gly Gly Ser Tyr  
 245 250 255  
 Arg Arg Pro Asp Ser Leu Phe Asp Pro Lys Leu Arg Asp Lys Lys Glu  
 260 265 270  
 Gln Arg Glu Thr Tyr Ile Glu Val Glu Gly Asp Asp Asp Arg Tyr Asp  
 275 280 285  
 Lys Lys Asn  
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<210> 20  
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 <213> Genomic dwf7 (Arabidopsis)  
  
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 tctcggtgga tctccgattc acatggcgcc ggataatgt tatctgtatgc agtttggta 180  
 cgaaacctct ttttacaacc gaatcggttct gaggcatctt ttggccggcga atctatggga 240  
 acccttaccc cattttctcc agacatggct ccggaaattac ctgcgggaa ccctactata 300  
 cttcatctcc ggttccctct ggtgcttcta catctattac cttaaaatca acgtttaccc 360  
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 gtggatagtt catgtttgca tttatttgatt atttggcat attctccatc taagggattg 540  
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 tctgtttgc ttccatgtca attccatcaa taaaggctat gcgttgcac atgtttgg 780  
 caatgaaggc tatgccatgg tacactcttc ttccaactgt ctccgagagt atgattgaac 840  
 gtgggtggac caaatgtttt gctagcatag acgaattcgg ctggattctg tattttgttt 900  
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atacactctc tccatggcc ggtaagtgtt ttcaagttgt tcttcattttg ttcttgtaaa 1080  
agattggtag catttagttt cttaccagaa aagactttgt cagcagctgc ttgtactcca 1140  
aatcacattt tgcatccatt atccataaag taaccagaaa ggctagaatt atataaatgt 1200  
cagctgcatt acttcacata tgtcagagag acttctgact taaccagagt ttagatctt 1260  
gtgtttctct tctggctcg gactgattgg aaatgacgag aagttttt atctacttc 1320  
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<210> 21  
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20 25 30  
  
Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu Ala  
35 40 45  
  
Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile  
50 55 60  
  
Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr  
65 70 75 80  
  
Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro  
85 90 95  
  
Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly  
100 105 110  
  
Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr  
115 120 125  
  
Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr  
130 135 140  
  
Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu  
145 150 155 160  
  
His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe  
165 170 175

Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro  
180 185 190

His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile  
195 200 205

Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys  
210 215 220

Ile	His	Gly	Asn	Ile	Trp	Pro	Val	Met	Gly	Ala	Gly	Tyr	His	Thr	Ile
225					230				235						240

His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp Met  
245 250 255

Asp	Trp	Met	Phe	Gly	Ser	Leu	Arg	Asp	Pro	Leu	Leu	Glu	Glu	Asp	Asp
			260				265					270			

Asn Lys Asp Ser Phe Lys Lys Ala Glu  
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<212> DNA  
<213> Genomic HDF7
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ttttcagttt gttttttttt agttttgtt aaaggatttgtt agcatttagt ttcttaccag 180  
aaaagacttt gtcagcagct gcttgtactc caaatcacat tttgcattcc ttatccataa 240  
agtaaccaga aaggcttagaa ttatataat gtcagctgca ttacttcaca tatgtcagag 300  
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cccagtagac gggatactta aggctgtacc gcatgtgata gcgcgtttat agtgcattttttt 540  
catttcaccaa cttttttttt atgaaagcga tatggacggc gaacatccat 600  
gactgcattcc atggcaacat ctggccagta atgggtgcag gataccatac gataccacac 660  
acgacatatac agcataacta tggtcattat accatatgga tggattggat gtttggctct 720  
cttagggatc ctcttttaga agaagatgac aacaaagaca gcttcaagaa agcagatgaa 780  
gaatgccccat ttgggtttttt ttcttctgtt ttgtcttgc ttgttgc ttgttgc 840  
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ccaaatttca aagatctcac caatcaaaat gttttttttt gttttttttt gttttttttt 1140  
gttaatccgt ctgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200  
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tagtaaacgc aattttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1320  
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Trp Glu Pro Leu Pro His Phe Leu Gln Thr Trp Leu Arg Asn Tyr Leu  
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Ala Gly Asn Ile Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr  
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Thr Arg Lys Ala Met Leu Leu Gln Ile Tyr Val Ala Met Lys Ala Met  
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Cys Phe Leu Tyr Ile Ala Leu Tyr Leu Val Leu Val Glu Phe Met Ile  
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 Tyr Trp Val His Lys Glu Leu His Asp Ile Lys Phe Leu Tyr Lys His  
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 Cys Ile His Gly Asn Ile Trp Pro Ile Met Gly Ala Gly Tyr His Thr  
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 Ile His His Thr Thr Tyr Lys His Asn Tyr Gly His Tyr Thr Ile Trp  
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Gly Thr Leu Leu Tyr Phe Ile Ser Gly Phe Leu Trp Cys Phe Tyr Ile  
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Tyr Tyr Leu Lys Ile Asn Val Tyr Leu Pro Lys Asp Ala Ile Pro Thr  
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Ile Lys Ala Met Arg Leu Gln Met Phe Val Ala Met Lys Ala Met Pro  
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Trp Tyr Thr Leu Leu Pro Thr Val Ser Glu Ser Met Ile Glu Arg Gly  
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Trp Thr Lys Cys Phe Ala Ser Ile Asp Glu Phe Gly Trp Ile Leu Tyr  
115 120 125

Phe Val Tyr Ile Ala Ile Tyr Leu Val Phe Val Glu Phe Gly Ile Tyr  
130 135 140

Trp Met His Arg Glu Leu His Asp Ile Lys Pro Leu Tyr Lys Tyr Leu  
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His Ala Thr His His Ile Tyr Asn Lys Gln Asn Thr Leu Ser Pro Phe  
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Ala Gly Leu Ala Phe His Pro Val Asp Gly Ile Leu Gln Ala Val Pro  
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His Val Ile Ala Leu Phe Ile Val Pro Ile His Phe Thr Thr His Ile  
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Gly Leu Leu Phe Met Glu Ala Ile Trp Thr Ala Asn Ile His Asp Cys  
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Ile His Gly Asn Ile Trp  
225 230